

General Description References Links Keywords Sequence

General information

www.uniprot.org **Q12563**
 Entry name **Q12563**
 Accession number **Q12563**
 Created TrEMBLrel. 01, 1-NOV-1996
 Sequence update TrEMBLrel. 01, 1-NOV-1996
 Annotation update TrEMBLrel. 25, 1-OCT-2003

Description and origin of the Protein

Description Alpha-mannosidase (EC 3.2.1.113).
 Organism source *Aspergillus phoenicis*.
 Taxonomy Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; Aspergillus.
 NCBI TaxID 5063

References

- [1] Inoue,T., Yoshida,T., Ichishima,E.,
Molecular cloning and nucleotide sequence of the 1,2-alpha-D- mannosidase gene
***Aspergillus saitoi* and expression of the gene in yeast cells.**
 (1995) *Biochim. Biophys. Acta* **1253**:141-145
 Position SEQUENCE FROM N.A.
 Medline 96106423
 PubMed 8519794

Database cross-references

EMBL D49827; BAA08634.1; -.
 HSSP P31723; 1KRE.
 GO GO:0016020; C:membrane; IEA.
GO:0005509; F:calcium ion binding; IEA.
GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
GO:0004571; F:mannosyl-oligosaccharide 1,2-alpha-mannosid...; IEA.
GO:0005975; P:carbohydrate metabolism; IEA.
GO:0006487; P:N-linked glycosylation; IEA.
 InterPro IPR001382; Glyco_hydro_47.
 Pfam PF01532; Glyco_hydro_47; 1.
 PRINTS PR00747; GLYHDLASE47.
 ProDom PD003239; Glyco_hydro_47; 1.

Keywords

Glycosidase; Hydrolase;

Sequence information

Length: **513 aa**, molecular weight: **55874 Da**, CRC64 checksum: **0FDAB2CB27E93724**

MHLPSLSLSL	TALAIASPSA	AYPHFGSSQP	VLHSSSDTTQ	SRADAIKAAF	SHAWDGYLQY	60
AFPHDELHPV	SNGYGDSRNG	WGASAVDALS	TAVIMRNATI	VNQILDHVGK	IDYSKTNTTV	120
SLFETTIRYL	GGMLSGYDLL	KGPVSDLVQN	SSKIDVLLTQ	SKNLADVLKF	AFDTPSGVPY	180
NNLNITSGGN	DGAKTNGLAV	TGTLALEWTR	LSDLTGDDTY	ADLSQKAESY	LLNPQPKSAE	240
PFPGLVGSNI	NISNGQFTDA	QVSWNGGDDS	YYEYLIKMYV	YDPKREGLYK	DRWVAAAQST	300
MQHLASHPSS	RPDLTFLASY	NNGTLGLSSQ	HLTCFDGGSF	LLGGTVLNRT	DFINFGLDLV	360
SGCHDTYNST	LTGIGPESFS	WDTSDIPSSQ	QSLYEKAGFY	ITSGAYILRP	EVIESFYAW	420
RVTGQETYRD	WIWSAFSAVN	DYCRTSSGFS	GLTDVNAANG	GSRYDNQESF	LFAEVMKYSY	480
MAFAEDAAWQ	VQPGSGNQFV	FNTEAHPVRV	SST			513

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